

10/697,527

STN

March 29, 2007

=> fil reg
FILE 'REGISTRY' ENTERED AT 15:27:15 ON 29 MAR 2007
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STRUCTURE FILE UPDATES: 28 MAR 2007 HIGHEST RN 928615-67-2
DICTIONARY FILE UPDATES: 28 MAR 2007 HIGHEST RN 928615-67-2

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predicted properties as well as tags indicating availability of
experimental property data in the original document. For information
on property searching in REGISTRY, refer to:

<http://www.cas.org/ONLINE/UG/regprops.html>

=> d que 18
L1 4 SEA FILE=REGISTRY ABB=ON PLU=ON CTATGAGGCGGAGGTTGAAG/SQSN
L2 4 SEA FILE=REGISTRY ABB=ON PLU=ON TGCGGTGCTCTTCCATTT/SQSN
L3 5 SEA FILE=REGISTRY ABB=ON PLU=ON CCAACCGTGCTATTAGTCATTC/SQSN
L4 5 SEA FILE=REGISTRY ABB=ON PLU=ON CAATGCAGGCCCTCCTAAC/SQSN
L8 18 SEA FILE=REGISTRY ABB=ON PLU=ON (L1 OR L2 OR L3 OR L4) AND
SQL<101

=> d 18 rn cn sql kwic nte lc tot

L8 ANSWER 1 OF 18 REGISTRY COPYRIGHT 2007 ACS on STN
RN 918838-29-6 REGISTRY
CN DNA, d(C-A-A-T-G-C-A-G-G-C-C-C-T-C-C-T-A-A-C) (CA INDEX NAME)
OTHER NAMES:
CN 21: PN: FR2888241 SEQID: 30 claimed DNA
SQL 19
SQL 19

SEQ 1 caatgcaggc cctcctaac
=====

HITS AT: 1-19

RELATED SEQUENCES AVAILABLE WITH SEQLINK

LC STN Files: CA, CAPLUS

L8 ANSWER 2 OF 18 REGISTRY COPYRIGHT 2007 ACS on STN
RN 918838-28-5 REGISTRY
CN DNA, d(C-C-A-A-C-C-G-T-G-C-T-A-T-T-A-G-T-C-A-T-T-C) (CA INDEX NAME)
OTHER NAMES:
CN 20: PN: FR2888241 SEQID: 29 claimed DNA
SQL 22
SQL 22

SEQ 1 ccaaccgtgc tattagtcac tc
===== ==
HITS AT: 1-22

RELATED SEQUENCES AVAILABLE WITH SEQLINK

LC STN Files: CA, CAPLUS

L8 ANSWER 3 OF 18 REGISTRY COPYRIGHT 2007 ACS on STN
RN 908626-85-7 REGISTRY
CN DNA, d(C-A-A-T-G-C-A-G-G-C-C-C-T-C-C-T-A-A-C) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1250: PN: WO2006094360 SEQID: 1250 claimed DNA
SQL 19
SQL 19

SEQ 1 caatgcaggc cctcctaac
===== ==
HITS AT: 1-19

RELATED SEQUENCES AVAILABLE WITH SEQLINK

LC STN Files: CA, CAPLUS

L8 ANSWER 4 OF 18 REGISTRY COPYRIGHT 2007 ACS on STN
RN 908626-84-6 REGISTRY
CN DNA, d(C-C-A-A-C-C-G-T-G-C-T-A-T-T-A-G-T-C-A-T-T-C) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1249: PN: WO2006094360 SEQID: 1249 claimed DNA
SQL 22
SQL 22

SEQ 1 ccaaccgtgc tattagtcac tc
===== ==
HITS AT: 1-22

RELATED SEQUENCES AVAILABLE WITH SEQLINK

LC STN Files: CA, CAPLUS

L8 ANSWER 5 OF 18 REGISTRY COPYRIGHT 2007 ACS on STN
RN 908626-29-9 REGISTRY
CN DNA, d(T-G-C-G-G-T-G-C-T-C-T-T-C-C-A-T-T-T) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1190: PN: WO2006094360 SEQID: 1190 claimed DNA
SQL 18
SQL 18

SEQ 1 tgcggtgctc ttccattt
===== ==
HITS AT: 1-18

RELATED SEQUENCES AVAILABLE WITH SEQLINK

LC STN Files: CA, CAPLUS

L8 ANSWER 6 OF 18 REGISTRY COPYRIGHT 2007 ACS on STN
RN 908626-28-8 REGISTRY
CN DNA, d(C-T-A-T-G-A-G-G-C-G-G-A-G-G-T-T-G-A-A-G) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1189: PN: WO2006094360 SEQID: 1189 claimed DNA
SQL 20
SQL 20

SEQ 1 ctatgagcg gaggttgaag

=====

HITS AT: 1-20

RELATED SEQUENCES AVAILABLE WITH SEQLINK

LC STN Files: CA, CAPLUS

L8 ANSWER 7 OF 18 REGISTRY COPYRIGHT 2007 ACS on STN

RN 900818-89-5 REGISTRY

CN DNA, d(C-A-A-T-G-C-A-G-G-C-C-C-T-C-C-T-A-A-C) (9CI) (CA INDEX NAME)

SQL 19

SQL 19

SEQ 1 caatgcaggc cctcctaac

=====

HITS AT: 1-19

RELATED SEQUENCES AVAILABLE WITH SEQLINK

LC STN Files: CA, CAPLUS

L8 ANSWER 8 OF 18 REGISTRY COPYRIGHT 2007 ACS on STN

RN 900818-88-4 REGISTRY

CN DNA, d(C-C-A-A-C-C-G-T-G-C-T-A-T-T-A-G-T-C-A-T-T-C) (9CI) (CA INDEX NAME)

SQL 22

SQL 22

SEQ 1 ccaaccgtgc tattagtcac tc

=====

HITS AT: 1-22

RELATED SEQUENCES AVAILABLE WITH SEQLINK

LC STN Files: CA, CAPLUS

L8 ANSWER 9 OF 18 REGISTRY COPYRIGHT 2007 ACS on STN

RN 682702-93-8 REGISTRY

CN GenBank AR493064 (9CI) (CA INDEX NAME)

SQL 19

SQL 19

SEQ 1 caatgcaggc cctcctaac

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HITS AT: 1-19

RELATED SEQUENCES AVAILABLE WITH SEQLINK

LC STN Files: GENBANK

L8 ANSWER 10 OF 18 REGISTRY COPYRIGHT 2007 ACS on STN

RN 682702-92-7 REGISTRY

CN GenBank AR493063 (9CI) (CA INDEX NAME)

SQL 22

SQL 22

SEQ 1 ccaaccgtgc tattagtcac tc

=====

HITS AT: 1-22

RELATED SEQUENCES AVAILABLE WITH SEQLINK

LC STN Files: GENBANK

L8 ANSWER 11 OF 18 REGISTRY COPYRIGHT 2007 ACS on STN

RN 682701-99-1 REGISTRY
CN GenBank AR492970 (9CI) (CA INDEX NAME)
SQL 18
SQL 18

SEQ 1 tgcggtgctc ttccattt
=====

HITS AT: 1-18

RELATED SEQUENCES AVAILABLE WITH SEQLINK

LC STN Files: GENBANK

L8 ANSWER 12 OF 18 REGISTRY COPYRIGHT 2007 ACS on STN
RN 682701-98-0 REGISTRY
CN GenBank AR492969 (9CI) (CA INDEX NAME)
SQL 20
SQL 20

SEQ 1 ctatgaggcg gaggttgaag
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HITS AT: 1-20

RELATED SEQUENCES AVAILABLE WITH SEQLINK

LC STN Files: GENBANK

L8 ANSWER 13 OF 18 REGISTRY COPYRIGHT 2007 ACS on STN
RN 217873-63-7 REGISTRY
CN GenBank A58956 (9CI) (CA INDEX NAME)
SQL 18
SQL 18

SEQ 1 tgcggtgctc ttccattt
=====

HITS AT: 1-18

RELATED SEQUENCES AVAILABLE WITH SEQLINK

LC STN Files: GENBANK

L8 ANSWER 14 OF 18 REGISTRY COPYRIGHT 2007 ACS on STN
RN 217873-62-6 REGISTRY
CN GenBank A58955 (9CI) (CA INDEX NAME)
SQL 20
SQL 20

SEQ 1 ctatgaggcg gaggttgaag
=====

HITS AT: 1-20

RELATED SEQUENCES AVAILABLE WITH SEQLINK

LC STN Files: GENBANK

L8 ANSWER 15 OF 18 REGISTRY COPYRIGHT 2007 ACS on STN
RN 186398-19-6 REGISTRY
CN DNA, d(C-A-A-T-G-C-A-G-G-C-C-C-T-C-C-T-A-A-C) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Deoxyribonucleic acid, d(C-A-A-T-G-C-A-G-G-C-C-C-T-C-C-T-A-A-C)
SQL 19
SQL 19

SEQ 1 caatgcaggc cctcctaac

=====

HITS AT: 1-19

RELATED SEQUENCES AVAILABLE WITH SEQLINK

LC STN Files: CA, CAPLUS, USPAT2, USPATFULL

L8 ANSWER 16 OF 18 REGISTRY COPYRIGHT 2007 ACS on STN

RN 186398-18-5 REGISTRY

CN DNA, d(C-C-A-A-C-C-G-T-G-C-T-A-T-T-A-G-T-C-A-T-T-C) (9CI) (CA INDEX NAME)

OTHER CA INDEX NAMES:

CN Deoxyribonucleic acid, d(C-C-A-A-C-C-G-T-G-C-T-A-T-T-A-G-T-C-A-T-T-C)

SQL 22

SQL 22

SEQ 1 ccaaccgtgc tattagtcac tc

=====

HITS AT: 1-22

RELATED SEQUENCES AVAILABLE WITH SEQLINK

LC STN Files: CA, CAPLUS, USPAT2, USPATFULL

L8 ANSWER 17 OF 18 REGISTRY COPYRIGHT 2007 ACS on STN

RN 186271-85-2 REGISTRY

CN DNA, d(T-G-C-G-G-T-G-C-T-C-T-T-C-C-A-T-T-T) (9CI) (CA INDEX NAME)

OTHER CA INDEX NAMES:

CN Deoxyribonucleic acid, d(T-G-C-G-G-T-G-C-T-C-T-T-C-C-A-T-T-T)

SQL 18

SQL 18

SEQ 1 tgcggtgctc ttccattt

=====

HITS AT: 1-18

RELATED SEQUENCES AVAILABLE WITH SEQLINK

LC STN Files: CA, CAPLUS, USPAT2, USPATFULL

L8 ANSWER 18 OF 18 REGISTRY COPYRIGHT 2007 ACS on STN

RN 186271-84-1 REGISTRY

CN DNA, d(C-T-A-T-G-A-G-G-C-G-G-A-G-G-T-T-G-A-A-G) (9CI) (CA INDEX NAME)

OTHER CA INDEX NAMES:

CN Deoxyribonucleic acid, d(C-T-A-T-G-A-G-G-C-G-G-A-G-G-T-T-G-A-A-G)

SQL 20

SQL 20

SEQ 1 ctatgaggcg gaggttgaag

=====

HITS AT: 1-20

RELATED SEQUENCES AVAILABLE WITH SEQLINK

LC STN Files: CA, CAPLUS, USPAT2, USPATFULL

=> fil hcap
 FILE 'HCAPLUS' ENTERED AT 15:28:08 ON 29 MAR 2007
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FILE COVERS 1907 - 29 Mar 2007 VOL 146 ISS 14
 FILE LAST UPDATED: 28 Mar 2007 (20070328/ED)

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This file contains CAS Registry Numbers for easy and accurate substance identification.

=> d que l9
 L1 4 SEA FILE=REGISTRY ABB=ON PLU=ON CTATGAGGCGGAGGTTGAAG/SQSN
 L2 4 SEA FILE=REGISTRY ABB=ON PLU=ON TGCGGTGCTCTTCCATTT/SQSN
 L3 5 SEA FILE=REGISTRY ABB=ON PLU=ON CCAACCGTGCTATTAGTCATTC/SQSN
 L4 5 SEA FILE=REGISTRY ABB=ON PLU=ON CAATGCAGGCCCTCCTAAC/SQSN
 L8 18 SEA FILE=REGISTRY ABB=ON PLU=ON (L1 OR L2 OR L3 OR L4) AND
 SQL<101
 L9 5 SEA FILE=HCAPLUS ABB=ON PLU=ON L8

=> d l9 ibib abs hitrn tot

L9 ANSWER 1 OF 5 HCAPLUS COPYRIGHT 2007 ACS on STN
 ACCESSION NUMBER: 2007:37402 HCAPLUS Full-text
 DOCUMENT NUMBER: 146:136355
 TITLE: Methods and primers for genotyping genetic polymorphisms in wheat strains using multiplex PCR for use in food products
 INVENTOR(S): Fournier, Regis; Boivin, Patrick; Salvo, Ludovic; Duret, Philippe
 PATENT ASSIGNEE(S): Institut Francais des Boissons de la Brasserie Malterie, Fr.; Grands Moulins de Paris
 SOURCE: Fr. Demande, 81pp.
 CODEN: FRXXBL
 DOCUMENT TYPE: Patent.
 LANGUAGE: French
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|------------------------|--|----------|-----------------|----------|
| ----- | ---- | ---- | ----- | ----- |
| FR 2888241 | A1 | 20070112 | FR 2005-7268 | 20050707 |
| PRIORITY APPLN. INFO.: | | | FR 2005-7268 | 20050707 |
| AB | The present invention provides methods and primers for genotyping genetic polymorphisms in wheat strains using multiplex PCR for use in food products. | | | |

The methods include profiling at least 5 loci, wherein nucleic acids may be obtained from grain, wheat malts, ground grains, wheatflour, bread, beer or other bakery products, French bread, pastries. Wheat varieties may be selected from Pytagor, Andalou, Isengrain, Bastide, Charger, Thesee, Claire, Croustry and Altria.

IT 918838-28-5 918838-29-6

RL: AGR (Agricultural use); ARG (Analytical reagent use); FFD (Food or feed use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)

(primer sequence; methods and primers for genotyping genetic polymorphisms in wheat strains using multiplex PCR for use in food products)

REFERENCE COUNT: 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 2 OF 5 HCAPLUS COPYRIGHT 2007 ACS on STN

ACCESSION NUMBER: 2006:945118 HCAPLUS Full-text

DOCUMENT NUMBER: 145:308086

TITLE: Multiplex PCR-based method of amplifying nucleic acids in a single closed-tube reaction

INVENTOR(S): Hayden, Matthew James

PATENT ASSIGNEE(S): Molecular Plant Breeding Nominees Ltd, Australia

SOURCE: PCT Int. Appl., 220pp.

CODEN: PIXXD2

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|---------------|--|----------|-----------------|----------|
| WO 2006094360 | A1 | 20060914 | WO 2006-AU318 | 20060310 |
| W: | AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, LY, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SM, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW | | | |
| RW: | AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LU, LV, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG, BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM | | | |

PRIORITY APPLN. INFO.: AU 2005-901191 A 20050311

AB The present invention provides a methods of amplifying nucleic acids using a multiplex, "closed-tube" PCR-based assay, in which reagents for all amplification reactions or stages (e.g., primers, enzyme, buffers) are present throughout said reactions or stages. In a first round of PCR, it is possible to specifically amplify nucleic acid at a locus of interest using an amount of tagged locus-specific primers suitable for performing exhaustive PCR (i.e., such that there is little or substantially no primer remaining after amplification). In a second round amplification, the first round amplification product is amplified using tag primers having lower melting temperature than the tagged locus-specific primers and annealed to the incorporated tag sequence in said first round amplification product at a lower annealing temperature than used in the first round. The present invention also provides a multiplex method of amplification, showing that it is possible to detect simple sequence repeats in nucleic acid from wheat, barley, apricot, cherry, cattle, sheep, and a fungus (*Rhynchosporium secalis*). The present

method also provides methods of characterizing or identifying individuals or for diagnosing a disease or disorder.

IT 908626-28-8 908626-29-9 908626-84-6
908626-85-7

RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)

(locus-specific primer for amplifying wheat nucleic acid; multiplex PCR-based method of amplifying nucleic acids in a single closed-tube reaction)

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 3 OF 5 HCAPLUS COPYRIGHT 2007 ACS on STN

ACCESSION NUMBER: 2006:47051 HCAPLUS Full-text

DOCUMENT NUMBER: 145:160261

TITLE: EST-derived SSR markers from defined regions of the wheat genome to identify *Lophopyrum elongatum* specific loci

AUTHOR(S): Mullan, Daniel J.; Platteter, Amanda; Teakle, Natasha L.; Appels, Rudi; Colmer, Timothy D.; Anderson, Joseph M.; Francki, Michael G.

CORPORATE SOURCE: School of Plant Biology, University of Western Australia, Crawley, WA, 6009, USA

SOURCE: Genome (2005), 48(5), 811-822
CODEN: GENOE3; ISSN: 0831-2796

PUBLISHER: National Research Council of Canada

DOCUMENT TYPE: Journal

LANGUAGE: English

AB *Lophopyrum elongatum*, a close relative of wheat, provides a source of novel genes for wheat improvement. Mol. markers were developed to monitor the introgression of *L. elongatum* chromosome segments into hexaploid wheat. Existing simple sequence repeats (SSRs) derived from genomic libraries were initially screened for detecting *L. elongatum* loci in wheat, but only 6 of the 163 markers tested were successful. To increase detection of *L. elongatum* specific loci, 165 SSRs were identified from wheat expressed sequence tags (ESTs), where their chromosomal positions in wheat were known from deletion bin mapping. Detailed sequence anal. identified 41 SSRs within this group as potentially superior in their ability to detect *L. elongatum* loci. BLASTN alignments were used to position primers within regions of the ESTs that have sequence conservation with at least 1 similar EST from another cereal species. The targeting of primers in this manner enabled 14 *L. elongatum* markers from 41 wheat ESTs to be identified, whereas only 2 from 124 primers designed in random positions flanking SSRs detected *L. elongatum* loci. Addition and ditelosomic lines were used to assign all 22 markers to specific chromosome locations in *L. elongatum*. Nine of these SSR markers were assigned to homoeologous chromosome locations based on their similar position in hexaploid wheat. The remaining markers mapped to other *L. elongatum* chromosomes indicating a degree of chromosome rearrangements, paralogous sequences and (or) sequence variation between the 2 species. The EST-SSR markers were also used to screen other wheatgrass species indicating further chromosome rearrangements and (or) sequence variation between wheatgrass genomes. This study details methodologies for the generation of SSRs for detecting *L. elongatum* loci.

IT 900818-88-4 900818-89-5

RL: AGR (Agricultural use); ARG (Analytical reagent use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)

(primer; EST-derived SSR markers and primers from defined regions of wheat genome to identify *Lophopyrum elongatum* specific loci and monitor

introgression)

REFERENCE COUNT: 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 4 OF 5 HCAPLUS COPYRIGHT 2007 ACS on STN

ACCESSION NUMBER: 1997:561669 HCAPLUS Full-text

DOCUMENT NUMBER: 127:273373

TITLE: Application of microsatellite markers to distinguish inter-varietal chromosome substitution lines of wheat (*Triticum aestivum* L.)

AUTHOR(S): Korzun, V.; Borner, A.; Worland, A. J.; Law, C. N.; Roder, M. S.

CORPORATE SOURCE: Institute fur Pflanzengenetik und Kulturpflanzenforschung, Gatersleben, D-06466, Germany

SOURCE: Euphytica (1997), 95(2), 149-155

CODEN: EUPHAA; ISSN: 0014-2336

PUBLISHER: Kluwer

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Wheat microsatellites (WMS) were used to test the authenticity of inter-varietal chromosome substitution lines developed using the varieties "Cappelle-Desprez" and "Bezostaya 1". The results demonstrated that the majority of the lines were correct. Microsatellites, with their abundance of polymorphic markers randomly distributed over the entire wheat genome, provided ideal tools for establishing the authenticity of cytogenetically developed genetic stocks of wheat.

IT 186271-84-1 186271-85-2

RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)

(nucleotide sequence of PCR primer for microsatellite WMS52; application of microsatellite markers to distinguish inter-varietal chromosome substitution lines of wheat (*Triticum aestivum* L.))

REFERENCE COUNT: 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L9 ANSWER 5 OF 5 HCAPLUS COPYRIGHT 2007 ACS on STN

ACCESSION NUMBER: 1997:127421 HCAPLUS Full-text

DOCUMENT NUMBER: 126:129381

TITLE: Microsatellite markers for wheat and the Triticeae and their uses

INVENTOR(S): Roeder, Marion; Plaschke, Jens; Ganai, Martin

PATENT ASSIGNEE(S): Institut fuer Pflanzengenetik und Kulturpflanzenforschung, Germany

SOURCE: Ger. Offen., 8 pp.

CODEN: GWXXBX

DOCUMENT TYPE: Patent

LANGUAGE: German

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

| PATENT NO. | KIND | DATE | APPLICATION NO. | DATE |
|--|------|----------|------------------|----------|
| ----- | ---- | ----- | ----- | ----- |
| DE 19525284 | A1 | 19970102 | DE 1995-19525284 | 19950628 |
| WO 9701567 | A2 | 19970116 | WO 1996-DE1185 | 19960627 |
| WO 9701567 | A3 | 19970313 | | |
| W: JP, US | | | | |
| RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE | | | | |
| EP 835324 | A2 | 19980415 | EP 1996-921885 | 19960627 |
| EP 835324 | B1 | 20020424 | | |

10/697,527

March 29, 2007

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE

| | | | | |
|------------------------|----|----------|------------------|-------------|
| AT 216730 | T | 20020515 | AT 1996-921885 | 19960627 |
| ES 2176467 | T3 | 20021201 | ES 1996-921885 | 19960627 |
| US 2002066118 | A1 | 20020530 | US 1998-983605 | 19980501 |
| US 6720137 | B2 | 20040413 | | |
| US 2004146898 | A1 | 20040729 | US 2003-697527 | 20031030 |
| PRIORITY APPLN. INFO.: | | | DE 1995-19525284 | A 19950628 |
| | | | WO 1996-DE1185 | W 19960627 |
| | | | US 1998-983605 | A3 19980501 |

AB Polymorphic microsatellite DNA markers of wheat that are of use in the typing and breeding of wheat and related Triticeae are described. Primer pairs for over 100 such markers are described.

IT 186271-84-1 186271-85-2 186398-18-5
186398-19-6

RL: AGR (Agricultural use); PRP (Properties); BIOL (Biological study);
USES (Uses)

(nucleotide sequence, primer for detection of microsatellite marker of wheat; microsatellite markers for wheat and Triticeae and their uses)

=> d his nofil

(FILE 'HOME' ENTERED AT 15:20:04 ON 29 MAR 2007)

FILE 'REGISTRY' ENTERED AT 15:20:14 ON 29 MAR 2007

| | | | | | |
|----|----|-----|--------|--------|------------------------------------|
| L1 | 4 | SEA | ABB=ON | PLU=ON | CTATGAGGCGGAGGTTGAAG/SQSN |
| L2 | 4 | SEA | ABB=ON | PLU=ON | TGCGGTGCTCTTCCATTT/SQSN |
| L3 | 5 | SEA | ABB=ON | PLU=ON | CCAACCGTGCTATTAGTCATTC/SQSN |
| L4 | 5 | SEA | ABB=ON | PLU=ON | CAATGCAGGCCCTCCTAAC/SQSN |
| L5 | 0 | SEA | ABB=ON | PLU=ON | L3 AND L4 |
| L6 | 0 | SEA | ABB=ON | PLU=ON | L1 AND (L2 OR L3 OR L4) |
| L7 | 0 | SEA | ABB=ON | PLU=ON | L2 AND (L3 OR L4) |
| L8 | 18 | SEA | ABB=ON | PLU=ON | (L1 OR L2 OR L3 OR L4) AND SQL<101 |

FILE 'HCAPLUS' ENTERED AT 15:27:08 ON 29 MAR 2007

L9 5 SEA ABB=ON PLU=ON L8

FILE 'REGISTRY' ENTERED AT 15:27:15 ON 29 MAR 2007

D QUE L8
D L8 RN CN SQL KWIC NTE LC TOT

FILE 'HCAPLUS' ENTERED AT 15:28:08 ON 29 MAR 2007

D QUE L9
D L9 IBIB ABS HITRN TOT